

Figure 1.

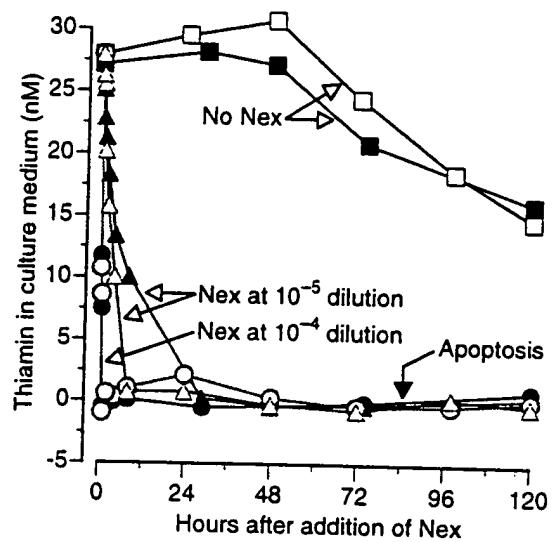


Figure 2.

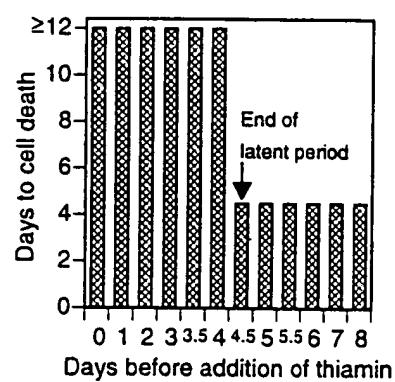


Figure 3.

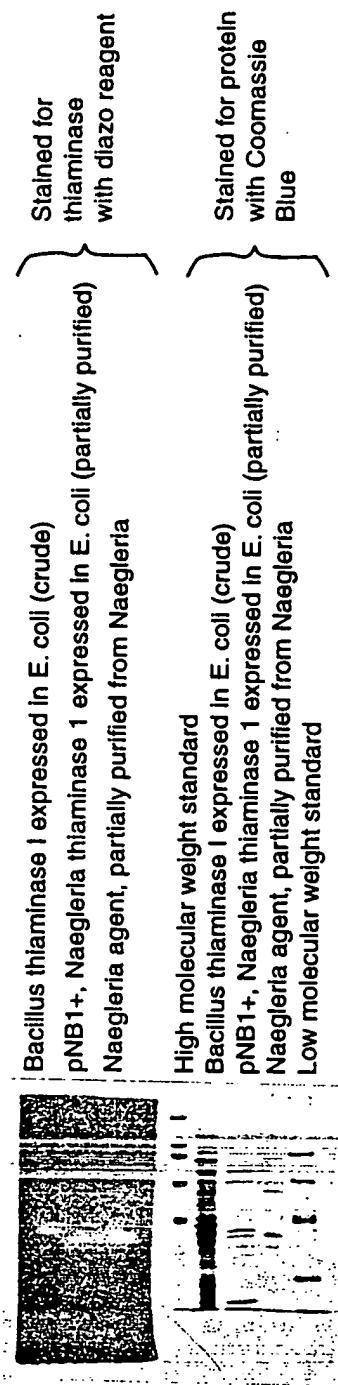


Figure 4.

(SEQ ID NO: 1)

1 ATGTCCACTC AACCAAAGAC ACTCACTGTT GGTCTCTTCC CATATCTTCC TTCTTGGAAAT
61 GAAAATGGCA ACGAAGTTAA ATTGATCAAT TTGATCAAGG ATGTTTGCC AACTCAGGTT
121 TCCGGATATA ATATCGAATA TACCGAATT GATTGTTACA GTGATGCTAG TCTTCAAAGT
181 CTTCCAGATG TTTTCTCAAC TGATAGCATT TCCCTCCAT ATCTTGTTC TTTGGGTGGT
241 GTCAAGAGTT TGGATGAATC ATTGGTCCGT GGTGTTACTG GTGATTTGCA TAGTTTGTT
301 TCCTCAAGTG CCTCTGTCAA TGGTTCCGT TATGGTTCC CACAATACTT GTGCTCAAAC
361 TTTTATTGTT CCTCACCAAA TGGTACTCAA CAAGCATCTT CCCTTTAGA ATTGGCTCAA
421 AAGGTTGGTT ATGAACAAAT TGTTTATCCA GATGTTGCCT CTTCTAGTTC TTTCACAGTT
481 TTCGGATTGT ATCAACAATT ACTCCAATCA TCATCATCAG CTGCAGTTGA TATCAAGGCC
541 TCTGATCTTC CACAATCTGG TGACCAAGTC ACAAGGATA TCACTCAAAA ATATAGAAC
601 ATTTTGGATT CAACAGTTGT TGCCTCTCAA AGAGAATATA TTAACTCTGT AAAGCAAGGT
661 AAACCAATT CAAACTACTA TGTCGGATAT AGTGAAAGTA TGTGTGAAAT TAAGGATATC
721 ATCAGAGATC ACAATACAA TGTTCAACTC ATTGGTACCT CTGATAAGCC ATACGTTTAT
781 ACTGATGTT TGGCTTGAA TTCCAATTG TGTGATGAAA AGCAAAGGT TGCTGTTGAA
841 GTTATCAAGA ATTTATTGAC TAATACTTTA GTTTGGACT TGTTGGTCT CGGATTAAC
901 CTCCCAGCCA ACAAGAATGG TATTGCTCAT TTGGCTAAAT CATCAAACCTT TTATGCTCAA
961 TTGAGCCAAC AATTCCGATGC CAAGGAAAGT GAAGTTAGAG TTTTGAGATG TGTTGACTTT
1021 GCTAACAAAGG AAGTTAAGAA TTGTGCTGGT GTCTTGAGAC CATTCTTCA ACATATTGCT
1081 GTTGCTACTT TGCGTTGTT GACTGCTGAC ACTGTCGAA AGGCTAAGAG TGGTCACCC
1141 GGTATGCCAA TTGGTATGTC ACCAATTGCC TATGTTTGT GGAAGTTCTT CTTCAAATCA
1201 TCTAAGGATG ATGTCAATTG GTTGAACAGA GATAGATTG TTTTGAGTAA TGGTCACGGT
1261 TGACATTGC TTTATGCCAT GTTGCACCTC ACTGATTGTA ACTTGAGTTT GGATGATCTC
1321 AAGAATTTC AAGGTTGCA TTCCAAGACT CCTGGTCACC CAGAATATGG TCACACTGAA
1381 GGTGTTGATG CTACTACTGG TCCATTGGGT CAAGGTGTTT GTAATGCTAT TGTTATGGCT
1441 CTCTCTGAAG CTCACTTGGC TGCTCGTTTC AATAAGGATG GACAAAATAT CTTTGATCAC
1501 CACACCTATG TTTTCCCTGG TGATGGTTGT TTGATGGAAC GTGTTGCTAT GGAAGGTCTC
1561 TCATTGCTG GTCACCAAAA GTTGAACAAG TTGATTGTTT TCTATGATGA CAATAGTATT
1621 ACTATTGATG GTAAGACTGA ATTGACCTTT ACTCAAATA CTCCAGAACT CATGAGAGGT
1661 TTTGGATGGC ACGTAATTGT TGTCGACAAG GCTGATAATG ACTTGGTTGG TATTAAGGAA
1721 GCTATTTGG AAGCTCACAC TGTTACTGAC AAGCCAATCA TGATCGTTG TAAGACTACA
1781 ATTGGTTATT CCTCAAAGGT TCAAGGTACT GCTAAGGTTG ACAGGTTCTCC ATTGGGTGCT
1841 GATGGATTGA AGAATTGAA GGAAACTTGT GGTTCACTG GTAATGATTT CTTCCATGTT
1901 CCAGAAATTG TCAGAAAGGA CTTTGCTACT GTCATTAATA GAAATAGTGA AAAGCTCT
1961 CAATGGAAGC AAGTTAAATC TGCCTATGAT ACCACTCATG CTACTGAATC CCAACTCCTC
2021 CAAAGAATGA TTAATCACGA ATTGGAAGGT GATGTTATGG AAAAGTTGCC AAAATACCTC
2081 GAACAAAAGA AGATIGCTAC CAGATCTACA TCTCAACAAG TTTTGAAATGC CATCTATCCA
2141 CTCATTCCTT CTCTCGTTGG TGGTTCAGCT GACTTGACTC CATCCAACCTT GACTGATGTA
2201 ACTGGATGTC AAGATTCCA ACCAAACAA AGAGTTGGTA GATATATCAG ATTGGTGTC
2261 CGTGAACATG CCATGGTTGC TATTGCCAAT GGTATTCTCT ATCATGGTGT TCTTAGAAC
2321 TATGTTGGTA CATTCTGAA CTTTGCTCA TATGCTTGG GTGCTATCAG ATTGAGTGCC
2381 TTGTCTGGTC TTCCAAATAT TTATGTTTC ACTCATGACA GTATTGGTCT TGGTCAAGAT
2441 GGTCCAACTC ACCAACCTGT TGAAGTTTA CCAATGTTGA TAGCCATTCC AAATCACATT
2521 GTTTTCAGAC CTGCTGATGG TAGAGAAACC AGTGGTGCTT ATTGTTGGGC TGTTCAATCA
2581 AAGAAGACTC CATCCTCAAT GATTCTTCT CGTCAAGATT TGCCACAATT GACTGGTACT
2641 GATATTTCAA AGGTTGCTTT GGGTGCTAT GTTATCCAAG GTGATGCTAC TCCTGATGTT
2701 GTCCTTGTG GTACTGGTTC TGAAGTTCC CTCATGGTTG AAGCTGCTGA AAAGTTGAAG
2761 GCTAACCTTA AGGTTAACGT TGTTCCATG CCAAGTTGGG AATTGTTGT TCGTCAATCA
2821 GAAGAATACA GGAAGACTGT CTTCCAGAT GGTATTCCAG TTGTCAGTGC CGAAGCTTCA
2881 TCAACCTTG GTTGGACAAG CTTTGCTCAC TATGCTGTTG GTATGACTAC TTTCGGTGCT
2941 AGTGCTGCTG CTGAAGAAGT TTACAAACTC CTCAAGATT CCTCAGACAA TGTTGCTGAA
3001 AAGGCCACCA AATTGGTTAC CAAGTATGGT AAGCAAGCTC CAAGACTCAG CTTGCTCTT
3061 GTTGGTGAAG AACTCTAA

Figure 5.

(SEQ ID NO: 2)

MSTQPKTLTVGLFPYLPWNENGNEVKLINLIKDVLPQVSGYNIEYTEFDCYSDASLQSLPDVFSTD SIFLPYLVS LGG
VKSLDES LVRGVGTGDLHSFVSSSASVNGSVYGFQYLCNFLLSPNGTQQASSLLEAQKVGYEQIVYPDVASSSSFTV
FGLYQQQLQSSSSAAVDIKASDLPQSGDQVNKDITQKYRTILDSTVVASQREYINSVKQGKPISNYVGYESMCEIKDI
IRDQQYNVQLIGTSDKPVYTDVLALNSNLCDEKQKVAVEVIKNLLNTLVLDLLGLGLTPANKNGIAHLAKSSNFYAQ
LSQQFDAKESEVRVLRCVDFANKEVKNCAGVRPFLQHIAVATRCLTADTVEKAKSGHPGMPIGMSPIAYVLWKF FKS
SKDDVNWLNRDRFVLNSHGCTLLYAMLHLTDCNLSLDDLKNFRSLHSKTPGHPEYGHTEGV DATTGPLGQGV CNAIGMA
LSEAHLAARFNKGQNI FDHHTYVFLGDCLMERVAMEGLSFAGHQKLNLIVFYDDNSITIDGKTELTFTQNTPEVMRG
FGWHVIVVDKADNDL VGIKEAILEAHTVTDKPIMIVCKTTIGYSSKVQGTAKVHGSPLGADGLKNLKETCGFTGNDFFHV
PEIVRKDFATVINRNSEKLSQWKQVKSAYDTTHATESQLLQRMINHELEGDVM EKLPKYLEQKKIATRSTSQQVLNAIYP
LIPSLVGGSA DLTPSNLTDVTGCQDFQPNNRVGRYIRFGVREHAMVAIANGILYHGVLR TYVGTFLNFASYALGAIRLSA
LSGLPNIYVFTHDSIGLGQDGPTHQPVEVLPMLIAIPNHIVFRPADGRETS GAYLWA VQSKKTPSSMILSRQDLPQLTGT
DISKVALGAYVIQGDA TPDVVLVGTGSEVSLMVEAAEKLKANLKVN VVSMPSWELFVRQSEYRKT VFPDGIPVVAEAS
STFGWTSFAHYAVGM TTFGASAAAEEVYKLLKITS DNVAEKATKLVT KYGKQAPRLSLSLVGEEL

Figure 6.

(SEQ ID NO: 3)

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ATGTCCACTCAACCAAAGACACTCACTGTTGGTCTTCCCATACTTCCTTCTTGAATGAAAATGGCAACGAAGTTAA  
ATTGATCAATTGATCAAGGATGTTGCCAAGTCAGGTTCCGGATATAATATCGAATATACCGAATTGATTGTTACA  
GTGATGCTAGTCTCAAAGTCTCAGATGTTCTCAACTGATAGCATTTCTTCCATACTTGTTCTTGGGTGGT  
GTCAAGAGTTGGATGAATCATTGGTCTGGTACTGGTATTCAGATGTTCTCAAGTGCCTGTCAA  
TGGTCCGTTATGGTTCCCACAATACTGTGCTCAAACCTTTATTGCTCACCAATGGTACTCAACAAGCATCTT  
CCCTTTAGAATTGGCTCAAAGGTTGTTATGAACAAATTGTTATCCAGATGTTGCCTCTCTAGTTCTTCACAGTT  
TTCGGATTGTATCAACAATTACTCCAATCATCATCAGCTGAGTTGATATCAAGGCCTCTGATCTTCCACAATCTGG  
TGACCAAGTCAACAAGGATACTCAAAATATAGAACCATTTGGATTCAACAGTTGTTGCCTCTCAAAGAGAATATA  
TTAACTCTGAAAGCAAGGTAACCAATTCTCAAACATGTTCAACTCATTGGTACCTCTGATAAGCCATACGTTACTGATGTTGGCTTGAA  
TTCCAATTGTTGATGAAAAGCAAAAGGTTGCTGTTGAAGTTATCAAGAATTATTGACTAATACTTAGTTGGACT  
TGTTGGGTCTCGGATTAACCTCCCAGCCAACAAGAATGGTATTGCTCATTTGGCTAAATCATCAAACCTTTATGCTCAA  
TTGAGCCAACAATTGATGCCAAGGAAAGTGAAGTTAGAGTTGAGATGTGTTGACTTGCTAACAGGAAGTTAAGAA  
TTGTGCTGGTCTTGAGACCATTCTT
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Figure 7. (SEQ ID NO: 3/SEQ ID NO: 4)

1/1 31/11
ATG TCC ACT CAA CCA AAG ACA CTC ACT GTT GGT CTC TTC CCA TAT CTT CCT TCT TGG AAT
Met ser thr gln pro lys thr leu thr val gly leu phe pro tyr leu pro ser trp asn

61/21 91/31
GAA AAT GGC AAC GAA GTT AAA TTG ATC AAT TTG ATC AAG GAT GTT TTG CCA ACT CAG GTT
glu asn gly asn glu val lys leu ile asn leu ile lys asp val leu pro thr gln val

121/41 151/51
TCC GGA TAT AAT ATC GAA TAT ACC GAA TTT GAT TGT TAC AGT GAT GCT AGT CTT CAA AGT
ser gly tyr asn ile glu tyr thr glu phe asp cys tyr ser asp ala ser leu gln ser

181/61 211/71
CTT CCA GAT GTT TTC TCA ACT GAT AGC ATT TTC CCA TAT CTT GTT TCT TTG GGT GGT
leu pro asp val phe ser thr asp ser ile phe leu pro tyr leu val ser leu gly gly

241/81 271/91
GTC AAG AGT TTG GAT GAA TCA TTG GTT CGT GGT GTT ACT GGT GAT TTG CAT AGT TTT GTT
val lys ser leu asp glu ser leu val arg gly val thr gly asp leu his ser phe val

301/101 331/111
TCC TCA AGT GCC TCT GTC AAT GGT TCC GTT TAT GGT TTC CCA CAA TAC TTG TGC TCA AAC
ser ser ser ala ser val asn gly ser val tyr gly phe pro gln tyr leu cys ser asn

361/121 391/131
TTT TTA TTG TCC TCA CCA AAT GGT ACT CAA CAA GCA TCT TCC CTT TTA GAA TTG GCT CAA
phe leu leu ser ser pro asn gly thr gln gln ala ser ser leu leu glu leu ala gln

421/141 451/151
AAG GTT GGT TAT GAA CAA ATT GTT TAT CCA GAT GTT GCC TCT TCT AGT TCT TTC ACA GTT
lys val gly tyg glu gln ile val tyg pro asp val ala ser ser ser phe thr val

481/161 511/171
TTC GGA TTG TAT CAA CAA TTA CTC CAA TCA TCA TCA GCT GCA GTT GAT ATC AAG GCC
phe gly leu tyg gln gln leu leu gln ser ser ser ala ala val asp ile lys ala

541/181 571/191
TCT GAT CTT CCA CAA TCT GGT GAC CAA GTC AAC AAG GAT ATC ACT CAA AAA TAT AGA ACC
ser asp leu pro gln ser gly asp gln val asn lys asp ile thr gln lys tyg arg thr

601/201 631/211
ATT TTG GAT TCA ACA GTT GTT GCC TCT CAA AGA GAA TAT ATT AAC TCT GTA AAG CAA GGT
ile leu asp ser thr val val ala ser gln arg glu tyg ile asn ser val lys gln gly

661/221 691/231
AAA CCA ATT TCA AAC TAC TAT GTC GGA TAT AGT GAA AGT ATG TGT GAA ATT AAG GAT ATC
lys pro ile ser asn tyg tyg val gln ser glu ser met cys glu ile lys asp ile

721/241 751/251
ATC AGA GAT CAA CAA TAC AAT GTT CAA CTC ATT GGT ACC TCT GAT AAG CCA TAC GTT TAT
ile arg asp gln gln tyg asp val gln leu ile gly thr ser asp lys pro tyg val tyg

781/261 811/271
ACT GAT GTT TTG GCT TTG AAT TCC AAT TTG TGT GAT GAA AAG CAA AAG GTT GCT GTT GAA
thr asp val leu ala leu asn ser asp leu cys asp glu lys gln lys val ala val glu

841/281 871/291
GTT ATC AAG AAT TTA TTG ACT AAT ACT TTA GTT TTG GAC TTG TTG GGT CTC GGA TTA ACT
val ile lys asn leu leu thr asp leu val asp leu leu gly leu leu thr l

901/301 931/311
CTC CCA GCC AAC AAG AAT GGT ATT GCT CAT TTG GCT AAA TCA TCA AAC TTT TAT GCT CAA
leu pro ala asn lys asn gly ile ala his leu ala lys ser ser asp phe tyg ala gln

961/321 991/331
TTG AGC CAA CAA TTC GAT GCC AAG GAA AGT GAA GTT AGA GTT TTG AGA TGT GTT GAC TTT
leu ser gln gln phe asp ala lys glu ser glu val arg val leu arg cys val asp phe

1021/341 1051/351
GCT AAC AAG GAA GTT AAG AAT TGT GCT GGT GTC TTG AGA CCA TTC CTT
ala asn lys glu val lys asn cys ala gly val leu arg pro phe leu

Figure 8-1.

Abbrev.	Genbank	Enzyme and Organism	
ScTKT1ct	P23254	Transketolase of <i>Saccharomyces cerevisiae</i>	
CpTKT7ct	Q42677	Transketolase of <i>Craterostigma plantagineum</i>	
EcTKT2ct	P33570	Transketolase of <i>Escherichia coli</i>	
BsTKTct	P45694	Transketolase of <i>Bacillus subtilis</i>	
MgTKT	P47312	Transketolase of <i>Mycoplasma genitalium</i>	
MjPTK1	Q58092	Transketolase of <i>Methanococcus jannaschii</i>	
BsTP	P45741	Thiaminase I precursor from <i>Bacillus thiaminolyticus</i>	
N40KAT	----->	Thiaminase I of <i>Naegleria gruberi</i> , aa 1-356	
ScTKT1ct	ADDVK---	QLKS KFGFPDKSFVVPQEVD-HYQK TILKPGVEANNKWNKL FSEY QKKFP	
CpTKT7ct	PKEAE---	ATRKNLGW-PYE PFPHV PDDV KK-HWSR HIAE-GAALES AWN AKFAEF QKKFP	
EcTKT2ct	EEEVA---	LARQ KLGW-HHPPF EI PKEI Y--HAWDAREK-GEKA QQSWNEKFAAY KKAHP	
BsTKTct	KEESK---	LTKEA YAWTYE EDFY VPSE VYE-HFAV AVKES GEKE QEWNAQ FAKY KEVYP	
MgTKT	EVDFQ---	LFEK RTNT-NFNFFNYPDSIYH-WFKQT VIERQKQI KEDYNNLLISLKD K-P	
MjPTK1	-----	-----	
BsTP	MSKVKGFIYKPLMVMLALLLVVSPAGAGAAHSDASSDITLKVAIYPYV PDPARFQAAVL	56	
N40KAT	MSTQP---	KTLTVGLFPYL---PS---WNENGNEVKLINLI KDVLPT-----	
ScTKT1ct	ELGAELARRLSGQLPANWESKLPTYTAKDSA---	VATRKLSETVLEDVYNQLP ELIGGS	112
CpTKT7ct	EEAADL KSI ITGELPT NWES IFPTY TPEN PG---	LPTR TL SHQ I L NGLGDV LPGL LGGS	
EcTKT2ct	QLAEEFTRRMSGGLPKDWEKTTQKYINELQANPAKIATRKASQNTLNAYGPMLPELLGGS		
BsTKTct	ELAEQLELAIKGELPKDWDQEV PYE-KGSS---	LASRASSGEV LNL GAKKI PFFFVGGS	
MgTKT	-LFKKFTNWIDSDFQALYLNQLDEKKVAKKD---	SATRN YLKDFLNQINNPN SNLYCLN	
MjPTK1	-----	-----	
BsTP	-MVKLSGVYKG-----MRKG YGET LIE LGKKY ENLV VLD		
N40KAT	DQWQRQEPGVKLEF-TDWDSYSADPPDLDV-----FVLD SIFL SHFV DAGYLLP-FGSQD		
	-----QVSGYNI EY-TEFD CYS DASLQLSPD---VFSTD SIFL PYLVSLGGVKS LDES LV		
ScTKT1ct	ADLTPSNL TRWKEALDFQPPSSGSGNYSGRYIRY GIREHAMGA---	IMNG ISAFG ANY KPYGG	172
CpTKT7ct	ADLTLNSM AFLKNSGDFQKSPGE-----	RNV KFGAREHAM GS-ICNGLALHSPGLLPYCA	
EcTKT2ct	ADLAPS NLTI WKG SVSL KEDPAGN-----	YIHYGVREFG MTA-IANGIA HHG-GFVPYTA	
BsTKTct	ADLAGS NKTTI KNA GDFTAVD YSG-----	KNF WFGVREFAM GA-ALNGM ALHG-GLRV FGG	
MgTKT	ADV SRS-CFIKIGDDNLHENPCS-----	RNIQIGI REFAM AT-IMNGM ALHG-GIKVMGG	
MjPTK1	ADLSGS-----TOTAMFAKEFPE-----	RFFNAGVAE QNMIG-MAAGLATTG-KIVFAS	
BsTP	IDQAEDVLPF ALQGAKRNGEVYGLP-----	QILCTNLLFYRK GDLKIGQVD NIYELYKKIG	
N40KAT	RGVTGDLHSFVSS SASVN GSVY GFP-----	QYLC SNF LLSS-----PNGTQQAS-SLLELAQ	
	.. .	* Catalytic Cys	
ScTKT1ct	TFLNFVS-YAAGAVR-LSALSGHPVIWVATHDSIGV-GE---	DG-PTHQPIET--LAHF	222
CpTKT7ct	TYFVFTD-YMRAAMR-ISALSKARVLYIMTHDSIGL-GE---	DG-PTHQPV EH--LASF	
EcTKT2ct	TFLMFVE-YARNAAR-MAALMKARQIMVYTHDSIGL-GE---	DG-PTHQAVEQ--LASL	
BsTKTct	TFFVFS D-YLRPAIR-LAALM GLPV TVV FTHDS IAV-GE---	DG-PTHEPVEQ--LASL	
MgTKT	TFLAFAD-YSKPAIR-LGALM NL PVF VVY THDSYQV-GG-----	DG-PTHQPYDQ--LPML	
MjPTK1	SFSM FASGRAWEI I RNL VAYPKL NVKIVATHAGITV-GE-----	DG-ASHQM CED-IAIM	
BsTP	TSHSE QIPPPQNKGLL INMAGGTTK ASMY LEAL IDV TGQY TEYD LPLD PLNDK VIRGL		
N40KAT	KVGYEQIVYPDVASSSSFTVFG LYQQLQSSSSAAV-----	DIKAS DLPQ SGD-QVN K	
	.. .	*	
	(SEQ ID NO: 12) Peptide A -> AS DLPQ SGD-QVN K		

Figure 8-2.

ScTKT1ct	RSLPNIQVWRPADGN-EVSAAYKNSLESKHTPSIIALSRQNLPQLEGS---SIESASKGG	278
CpTKT7ct	RAMPNILTLPADGN-ETAGAYRAAVQNGERPSILVLARQKLPQLPGT---SIEGVSKGG	
EcTKT2ct	RLTPNFSTWRPCDQV-EAAVGWLAVERHNGPTALILSRQNLAQVERTPD-QVKEIARGG	
BsTKTct	RAMPNLSLIRPADGN-ETAAAWKLAVQSTDHPTALVLTRQNLPIDQTSEALAGVEKG	
MgTKT	RAIENVCVFRPCDEK-ETCAGFNYGLLSQDQTTVLVLRQPLKSIDNTD-SLKTL-KGG	
MjPTK1	RAIPNMVVIAPTDYY-HTKNVIRTIAEYKG-PVYVRMPRRDTEIIYENEEEATFEIGKGK	
BsTP	RLLINMAGEKPSQYVPEDGDAYVRASWFAQ-GSGRAFIGYSESMMRMG---DYAEQVRFK	
N40KAT	DITQKYRTILDSTVV-ASQREYINSVKQGK-PISNYYVGYESMCEIK--DIIRDQQYN	

Peptide B -> TILDSTVV-ASQR (SEQ ID NO: 13)

ScTKT1ct	YVLQDVAN----PDIILVATGSEVSLSVEAAKTLAAKNIKARVVSLPDFFTFDKQPLE-	332
CpTKT7ct	YVISDNRGGNSKPDVILIGTGELEIAARAGDELKEGKKVRRVSLVCWELFAEQSEK-	
EcTKT2ct	YVLKDGG---KPDIIILATGSEMEITLQAAEKLAGEGRNVRRVSLPSTDIFDAQDEE-	
BsTKTct	YVVSKSKN--E-TPDALLIASGSEVGLAIEAQAEELAKENIDVSVSVSMPMSMDRFEKQSDE-	
MgTKT	YILLDRKQ----PDLIIAASGSEVQLAIEFEKVLTKQNVKVRILSVPNITLLLKQDEK-	
MjPTK1	ILVDG-----EDLTIIATGEEVPEALRAGEILKENGISAEEIVEMATIKPIDEEIICK	
BsTP	PISSSAG----QDIPLFYSDVVSVNSKTAHPELAKKLANVMASADTVEQALRPQADGQ	
N40KAT	VQLIGTS-----DKPYVYTDVLALNSN--LCDEKQKVAVEVIKNLLTNTLVLDLLG-	

ScTKT1ct	YRLSVPDPNVPI-MSVEVLATTCWGKYAH-----QSFGIDRGFGASGKAPEVFKFFGFTP	385
CpTKT7ct	YRETVPSPGTARVSVAGSTFGWERFIGP-KG--KAVGIDRGFGASAPAERLFKEFGITV	
EcTKT2ct	YRESVLPNSVAARVAVEAGIADYWKYVGL-KG--AIVGMTGYGESAPADKLFPPFGFTA	
BsTKTct	YKNEVLPADVKRLAIEMGSSFGWGKYTGL-EG--DVLGIDRGFGASAPGETIINEYGF	
MgTKT	YLNKSLFDANSSL-ITIEASSSYEWFCFKKY-VKNHAHLGAFSGESDDGDKVYQQKGFLN	
MjPTK1	SKDFVVTVEDHSIIGGLGGAVAEVIASNGLNKKLLRIGINDVFGRSRKADELLKYYGLDG	
BsTP	YPQYLLPARHQV-YEALMQDYPYIYSELQIVNK--PSNRVFRLGPEVRT-WLKDAKQVLP	
N40KAT	-LGTLTPANKNG-IAHLAKSSNFYAQLSQ-----QFDAKESEVRVLRCVDFANKEV	

Peptide C -> SSNFYQAQLSQ-----QFDAK (SEQ ID NO: 14)

ScTKT1ct	EGVAERAQKTIAYKGDKLISPLKKAF	412	(SEQ ID NO: 5)
CpTKT7ct	EAVVA-AAKEIC-----		(SEQ ID NO: 6)
EcTKT2ct	ENIVAKAHKVLGVKGA-----		(SEQ ID NO: 7)
BsTKTct	PNVNRVVKALINK-----		(SEQ ID NO: 8)
MgTKT	ERLMKIIFTSLRN-----		(SEQ ID NO: 9)
MjPTK1	ESIAKRIMEEMKKE-----		(SEQ ID NO: 10)
BsTP	EALGLTDVSSLAS-----		(SEQ ID NO: 11)
N40KAT	KNCAGVLRPFL-----		(SEQ ID NO: 4)